Download Data - Missing values - Experimental Design - Create DESeq2 object

Filtering - 0.5 CPM in at least 3 libraries - 50869 to 17057 genes

R and Rstudio
~ DESeq2
~gage/gageData

DEGS

- P Adj < 0.05
 - Abs(LFC) >= 2
 - Up: 1160 genes
 - Down: 1152 genes

- Pathway
 Analysis
- KEGG and GeneOntologypathways

Analysis of Results

- Our takeaways
- Comparison to orginal study
- -Comparison to current literature

Data Normalization

- VST transformation

EDA

- Data checks
 - PCA Plot
- Hierarchical Clustering